IMPLEMENTATION OF UNIFYING ACTIVE CONTOUR MODEL AND ITS APPLICATION FOR RECTAL TUMOR BOUNDARY DETECTION

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Abstract-**Boundary finding of rectal tumor in an ultrasound image is essential for quantification of tumor features. In this paper, we propose a novel unifying active contour model with integrated image region and gradient features. Region-based component added in the model, however, introduces a Gaussian Mixture Model (GMM) algorithm into the segmentation of the image and hence becomes less sensitive to noise. This paper focuses more on the implementation of the model in practical application and the application for rectal tumor boundary detection. The experimental results have shown the new model has more optimal performance for image segmentation and boundary finding than classical contour model.**
Keywords **- Active contour model, Rectal wall ultrasound image**

I. INTRODUCTION

Rectal cancer has emerged as one of the common diseases in developed countries. Rectal tumor is a special region with different gray level feature from balloon region and rectal muscular layers in a rectal ultrasound image [1]. The challenge from rectal tumor boundary detection is the non-homogeneity of tumor region. Therefore, low-level image processing methods are not suitable for performing the boundary detection. Some traditional high-level boundary detection algorithms, which depend on gradient feature of a image, as like snakes, point distribution model and level set, sometime also suffer from this difficulty because of some unstable features in the models [2]. However, region-based segmentation methods based on statistical algorithms are more suitable for this kind of area segmentation. A series of efforts have been done to integrate boundary and region information in one model for image segmentation and boundary detection [3][4][5]. In this paper, a unifying active contour model with region and gradient information is proposed and implemented to solve this kind of issue.

II. METHOD

A. Model

Our active contour model is set up based on the framework of Mumford-Shah model and redefined as,

$$E(U, K) = \iint |\nabla U(x, y)|^2 \, dxdy \; + \tag{1}$$
$$\iint (U(x, y) - I(x, y))^2 \, dxdy \; + length \; (K).$$

Consistent with the above three terms in (1), the active contour model consists of three main energy modules: the boundary-based energy module, region-based energy module and contour self-constraint energy module.

1) *Boundary-based energy module:* The energy module that decides the boundary finding of object or implementing image segmentation is based on the boundary information. Here, like traditional "snakes", we choose the gradient magnitude from an image as the boundary information of an object. The energy module corresponds to

$$E_{bnd}(v(x(s), y(s))) = \int - |\nabla I(x(s), y(s))|^2 \, ds \tag{2}$$

where $v(x, y) = v(x(s), y(s))$ is the vector expression of active contour, each vector represents a node on the contour. $I(x, y)$ represents image intensity. Thus, the image segmentation or object detection is to, within a certain capture range, find the object's boundary that has the minimum energy on the gradient magnitude field of the image.

2) *Region-based energy module:* Generally, the function of region-based energy is aimed at using this module to classify an image into a number of regions or classes. It has the capability of classifying an image into several sub-regions based on their intensity features or more specially based on their statistical features. An important principle is that the variation of the features in a given region is smaller than that between the regions, even though there exists the non-homogeneity in the interior of the region.

In this paper, the boundary finding of a specific object can be considered a special case of image segmentation, which segments the object from its background image. The region-based energy is designed to maximize *a posterior* probability of the region information with a given intensity image and hence perform segmentation of the image. The region energy can be represented as,

$$E_{regn} = -\log\left(\prod_{(x,y)\in R_O} p_O(I(x,y)) \prod_{(x,y)\in R_B} p_B(I(x,y)) \right) \tag{3}$$
$$= - \iint_{(x,y)\in R_O} \log(p_O(I(x,y)))dxdy - \iint_{(s,y)\in R_B} \log(p_B(I(x,y)))dxdy$$

where R_O represents the interior region of the active contour and R_B the exterior region of the contour. For boundary finding of an object, as the rectal wall tumor, one initial contour (seed) with its corresponding probability distribution p_O and its background's probability p_B are needed. For multiple regions' segmentation, multiple seeds are needed to place on their respective regions.

3) *Internal energy module:* For the constraint of contour's feature, the concept from "snakes" that the tension and rigidity of the contour are constrained by its first and second derivatives is applied here. This module helps perform the constraint to the shape of the contour and is denoted by

$$E_{int}(v(s)) = \int ((\alpha(s)|v_s(s)|^2 + \beta(s)|v_{ss}(s)|^2)/2)ds \tag{4}$$

where $v_s(s)$ and $v_{ss}(s)$ are the first and second derivatives with respect to the arc length s, respectively, and $\alpha(s)$ as well as $\beta(s)$ are the corresponding weighting parameters.

Combining above three modules, a general energy model is represented as follow:

$$E(v(s)) = w_{bnd} \left[\int - \left| \nabla I(x(s), y(s)) \right|^2 ds \right] +$$

$$w_{regn} \left[- \iint_{(x,y) \in R_O} \log(p_O(I(x,y))) dx dy - \iint_{(x,y) \in R_B} \log(p_B(I(x,y))) dx dy \right] + \quad (5)$$

$$\int ((\alpha(s)|v_s(s)|^2 + \beta(s)|v_{ss}(s)|^2)/2) ds$$

where w_{bnd}, w_{regn} are the weighting parameters.

B. Gaussian mixture model (GMM)

In some situations of image segmentation, an object region is not fully homogeneous, because of speckle or internal reflectivity. Like rectal tumors in ultrasound images, the features from their gray level histogram demonstrate that the pixel intensity of tumor region doesn't conform to a uniform distribution or a single Gaussian distribution.

For the purpose of representing an object's statistical feature from its gray value, a GMM consisting of three weighted Gaussian components (1 dimension) is built. Choosing three Gaussian components is based on the consideration that too many components would naturally increase the computational complexity for the parameter estimation of the GMM. Three components are enough for accurate description of the object's gray-level statistical feature generally. The GMM is defined as

$$\begin{cases} p(I|\Phi) = \alpha_1 p_1(I|\mu_1, \sigma_1) + \alpha_2 p_2(I|\mu_2, \sigma_2) \\ + \alpha_3 p_3(I|\mu_3, \sigma_3) \\ \sum_{j=1}^{3} \alpha_j = 1 \end{cases} \quad (6)$$

There are nine parameters { α_1, α_2, α_3, μ_1, μ_2, μ_3, σ_1, σ_2, σ_3,} in this GMM, collectively expressed by Φ. How to estimate these parameters based on an obtained sample data set I from a seed is given in the following.

C. Parameter estimate of GMM by EM algorithm

A maximum-likelihood (ML) algorithm is applied for above parameter estimation. The EM algorithm, by an iterative procedure, is applied here to find the maximum-likelihood estimate of the parameters from an observed data set I when these data are considered as *incomplete data.* The EM algorithm consists of the following two iterative steps - E (Expectation) step and M (Maximization) Step. The E step is to find the expected value of the complete-data $\{I,Y\}$ likelihood function,

$$Q(\Phi, \Phi^{(i-1)}) = E[\ln p(I,Y|\Phi)|I, \Phi^{(i-1)}] \quad (7)$$

where $Y = \{Y_1, Y_2, ..., Y_i\}$ is called "latent data" or "missing data". Then, the M step is to maximize the above expectation by an iterative procedure and get the parameters Φ, as

$$\Phi^{(i)} = \arg \max_{\Phi} Q(\Phi, \Phi^{(i-1)}) \quad (8)$$

D. Implementation of the model

Dynamic programming approach [6] is applied here for the energy-minimizing active contour. The unifying active
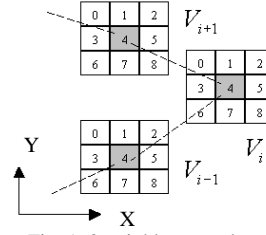

Fig. 1. 8-neighbor template of a node in an unifying active contour

contour consists of a series of nodes, which in sequence form a curve. Each node V_i has its own 8 neighbors, which construct a 9-point template (Fig. 1).

1) *Internal energy:* the continuity energy for each element inside the template can be computed as $E_{con}(V_{i,j}) = \left| d - \|V_{i,j} - V_{i-1,4}\| \right|$, $j = 0,..,8$, where d is the average distance between two neighboring nodes in the contour. The energy is finally represented by a normalized value as $E_{con}(V_{i,j}) = \left| d - \|V_{i,j} - V_{i-1,4}\| \right| / \max(E_{con}(V_i))$, where $\max(E_{con}(V_i))$ is the maximum in the neighbors of node V_i. The curvature energy for each element inside the template can be computed as $E_{cur}(V_{i,j}) = \left| V_{(i+1,4)} - 2V_{(i,j)} + V_{(i-1,4)} \right|^2$, $j = 0,..,8$. The energy is finally represented by a normalize value as $E_{cur}(V_{i,j}) = \left| V_{(i+1,4)} - 2V_{(i,j)} + V_{(i-1,4)} \right|^2 / \max(E_{cur}(V_i)$.

2) *Boundary energy:* The energy can be computed as $E_{bnd}(V_{i,j}) = (G_{min}(V_i) - G(V_{i,j}))/(G_{max}(V_i) - G_{min}(V_i))$, where $G_{min}(V_i)$ and $G_{max}(V_i)$ are minimum and maximum of image gradient values in the template. A threshold is set to avoid these two values are too near or equal. Thus, if ($G_{max}(V_i) - G_{min}(V_i)$)<threshold, $G_{min}(V_i)$ will be set as $G_{max}(V_i) - threshold$.

3) *Region energy:* The energy is using the results of GMM to judge whether the whole template region is inside the object region or background region in the image, thereby deciding the moving direction (outwards or inwards) of the current node. It is represented as:

$$E_{regn}(V_i) = \sum_{j=0,...8} prob(greylevel(V_{i,j}))/9 - threshold$$

where $prob(greylevel(V_{i,j}))$ is the probability of the current pixel's intensity in GMM. If $prob(greylevel(V_{i,j}))/9 > threshold$, it means the node is in the object region and needs to move outwards in the next step; otherwise, the node is in the background region and needs to move inwards in the next step. From the other two neighboring nodes and the current node, the normal of current node can be computed and its corresponding position (jR) in the template can be obtained too. Then, in the template, $E_{regn}(V_{i,jR})$ is given the obtained energy value; the others will be set zero.

Finally, the movement of a specific node is determined by the weighting sum of above three kinds of energy in the

template. The minimum energy point in the template is the next position of the node.

E. K-Means algorithm

A K-Means algorithm is implemented for clustering the input data by scanning the data set containing gray values of pixels from a delineated image region and serving for providing initial values needed by GMM-EM algorithm. The input data for the algorithm are data set (samples) to be clustered, number of clusters defined, and data dimension. An objective function is requested for setting the criteria of terminating the iterative process of clustering. A common process of the K-Means algorithm includes scanning the data, finding the distance of a sample and a cluster center, associating the sample with one cluster, updating the cumulative value of each cluster, updating the center of each cluster and judging the iterative criteria based on objective function. The output data are the center of each cluster and the value of the objective function.

F. Implementation of GMM and EM algorithm

In the proposed unify active contour model, the density function of gray values $\{I^n\}, n = 1,...,N$ is represented as a linear combination of 3 components of Gaussian model as:

$$p(I) = \sum_{j=1}^{3} p(I \mid j) P(j) \qquad (9)$$

where Gaussian density function (1D) is represented as

$$p(I \mid j) = \frac{1}{\left(2\pi\sigma_j^2\right)^{1/2}} \exp\left\{ -\frac{\|I - \mu_j\|^2}{2\sigma_j^2} \right\} \qquad (10)$$

The process of estimating the parameters in the GMM is carried out through maximizing the likelihood function of the gray-level data set. Usually, the likelihood maximization can be converted to a negative log likelihood minimization (also called error function), represented as:

$$e = -\ln L_j = -\sum_{n=1}^{N} \left\{ \ln \sum_{j=1}^{3} p(I^n \mid j) P(j) \right\} \qquad (11)$$

The minimization is implemented by the EM algorithm due to the simplicity of the EM algorithm and its guarantee of monotone decrease of the error function during the optimization. Therefore, the EM algorithm carries out the iterative process by the following formula to obtain the parameters of GMM while the error function arrives at its minimum or the number of iterative loop arrives at the predefined value.

$$\mu_j' = \sum_{n=1}^{N} P(j \mid I^n) x^n \Big/ \sum_{n=1}^{N} P(j / I^n) \qquad (12)$$

$$\left(\sigma_j'\right)^2 = \frac{1}{d} \frac{\sum_{n=1}^{N} P(j \mid I^n) \|I^n - \mu_j'\|}{\sum_{n=1}^{N} P(j \mid I^n)} \qquad (13)$$

$$P(j)' = \frac{1}{N} \sum_{n=1}^{N} P(j \mid I^n) \qquad (14)$$

The input data of GMM-EM model is data set of grey values, dimension of data, number of Gaussian components.

The output of the model is the means, variances and coefficients. The initial values of the means in the model are the ones obtained from the K-Means algorithm.

III. EXPERIMENTS AND RESULTS

In a rectal wall ultrasound image, a solid tumor usually appears black, for it is poorly reflective. The histogram of rectal tumor region shows that the tumor's gray level distribution occupies a lower range of a 256 gray level. The features from the histogram of a rectal tumor demonstrated that this region doesn't conform to a uniform distribution.

For implementing tumor boundary detection from ultrasound images, a unifying active contour model, consisting of internal energy, gradient energy and region energy, was set up. The region energy was represented by a GMM with three components of Gaussian distribution.

An application software was programmed by C++ language. Implementation of tumor boundary detection was one of the functions in the application software.

Several aided approaches, such as inserting a node and its corresponding template in the contour, deleting a redundant node, avoiding the contour going across itself etc., were built in the software for performing good deformation during the boundary detection.

One of the function pages related to the tumor boundary detection is shown in Fig. 2. An interactive tool was designed to help a user to define the seed inside the tumor region. First, the user needs to use mouse to click points on the image, which can be in sequence connected to form a closed contour (seed) as an initial position of the unifying active contour. Then, the algorithm can collect all pixels inside the contour as a representative of the tumor region. The region information, GMM and its parameters can be created from these pixels' gray level by K-Means algorithm and EM algorithm. After the unifying active contour is set up, a detection process will start. The active contour will be guided by internal energy, gradient energy and region energy and final find the boundary of the tumor.

Surgeons and researchers were invited to use the software and evaluate the results of tumor boundary detection on 16 rectal ultrasound images. A preliminary conclusion was that the results were acceptable in clinic, but a further quantitative evaluation and assessment would be carried out. Figure 3 shows 8 typical results of the tumor boundaries (white contours in the Figures) detected by the software.

IV. DISCUSSION

From the experimental results, the model shows robust dynamic behavior. The feature of convergence velocity is tested regarding our algorithm with the traditional snakes' and balloon snakes' algorithm. Compared to the traditional one, the proposed algorithm doesn't need user to put the initial active contour in the capture range of the desired boundary, therefore, reduce the amount of work for a user. Compared with the balloon snakes, usually, an iterative number of the algorithm is less if two active contours are initialized at the same position. The stability of the model is improved too.
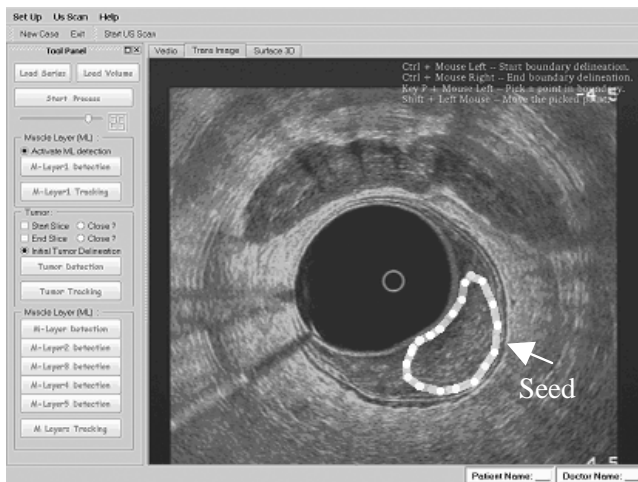
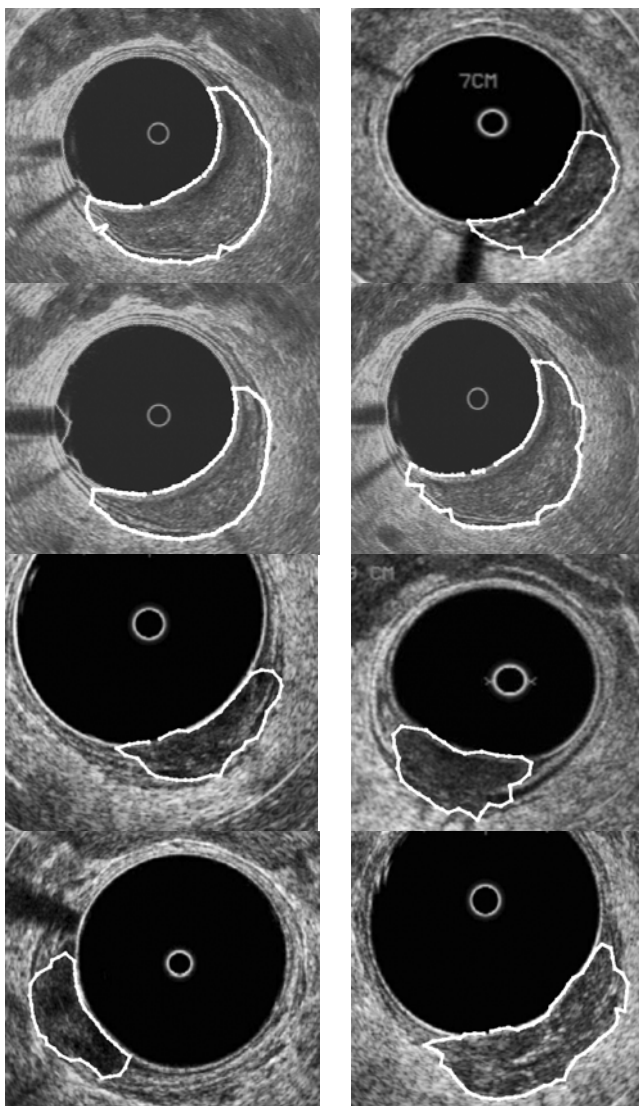Fig. 2. GUI of the software and initial seed of tumor

Fig. 3. Some typical results of tumor boundary detection

The clinical image trials has shown the addition of region-based feature based on GMM gives more flexibility for the active contour model than the "snake" algorithm and accelerates the velocity of the convergence. Compared with other region-based algorithm, the GMM applied in the algorithm provides a more accurate description of the tumor region. It doesn't need the initial contour to be placed at the gradient capture range of the desired boundary, but more emphasizes the effect of the region information from the initial active contour. The procedure of boundary finding is a combined effect of the internal energy, region energy and gradient energy. One of the important features is that our algorithm is constructed by Gaussian Mixture Model and solved by EM algorithm, thereby ensuring the accurate statistical description of a seed region.

Some shortcomings are also existed with this unifying active contour model. If the initial active contour is place on a wrong region, the incorrect statistical feature will be obtained and will influence the performance of the active contour. The sensitivity from weighting coefficients is also existed like that in other snake algorithms.

V. CONCLUSION

An active contour model unifying the region-based and gradient-based features from the image is proposed and implemented in the application software for rectal tumor boundary finding. A GMM is applied in the model for accurate representation of the region information.

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